GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 11, 2006, 22:41:25 ; Search time 189.875 Seconds
                                             (without alignments)
                                             458.231 Million cell updates/sec

Title: US-10-072-159-1
Perfect score: 31
Sequence: 1 FXXXXXXXXXXXXXXXXXXFXXXXXGXYXFXX 31

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10072159/runat_10082006_161645_23320/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss08 -USER=US10072159_@CGN_1_1_252_@runat_10082006_161645_23320
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                  1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                  2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                  3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                  4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                  5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                  6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                  7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                  8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                  9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                  10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	23	74.2	758	5	US-09-974-300-2197	Sequence 2197, Ap
c	2	23	74.2	888	3	US-09-937-862B-23	Sequence 23, Appl
	3	23	74.2	1206	3	US-09-543-681A-1133	Sequence 1133, Ap
	4	23	74.2	2101	4	US-10-094-749-1399	Sequence 1399, Ap
c	5	23	74.2	3219	3	US-09-614-221A-470	Sequence 470, App
c	6	22	71.0	377	3	US-09-621-976-11394	Sequence 11394, A
c	7	22	71.0	505	3	US-09-533-559-1234	Sequence 1234, Ap
c	8	22	71.0	525	3	US-09-949-016-5412	Sequence 5412, Ap
	9	22	71.0	601	3	US-09-949-016-48909	Sequence 48909, A
	10	22	71.0	601	3	US-09-949-016-48910	Sequence 48910, A
	11	22	71.0	601	3	US-09-949-016-49081	Sequence 49081, A
	12	22	71.0	601	3	US-09-949-016-49082	Sequence 49082, A
	13	22	71.0	601	3	US-09-949-016-49253	Sequence 49253, A
	14	22	71.0	601	3	US-09-949-016-49254	Sequence 49254, A
	15	22	71.0	601	3	US-09-949-016-49429	Sequence 49429, A
	16	22	71.0	601	3	US-09-949-016-49430	Sequence 49430, A
c	17	22	71.0	601	3	US-09-949-016-151201	Sequence 151201,
	18	22	71.0	601	3	US-09-949-016-160930	Sequence 160930,
c	19	22	71.0	601	3	US-09-949-016-177580	Sequence 177580,
	20	22	71.0	700	3	US-09-735-271-217	Sequence 217, App
c	21	22	71.0	714	3	US-09-270-767-3438	Sequence 3438, Ap
c	22	22	71.0	714	3	US-09-270-767-18720	Sequence 18720, A
c	23	22	71.0	726	3	US-09-533-559-5611	Sequence 5611, Ap
c	24	22	71.0	794	3	US-09-533-559-6598	Sequence 6598, Ap
c	25	22	71.0	801	3	US-09-252-991A-1475	Sequence 1475, Ap
	26	22	71.0	801	3	US-09-710-279-2065	Sequence 2065, Ap
	27	22	71.0	807	3	US-09-252-991A-1702	Sequence 1702, Ap
	28	22	71.0	879	3	US-09-134-001C-1305	Sequence 1305, Ap
	29	22	71.0	918	3	US-09-328-352-1943	Sequence 1943, Ap
	30	22	71.0	1083	3	US-09-270-767-6118	Sequence 6118, Ap
	31	22	71.0	1083	3	US-09-270-767-21400	Sequence 21400, A
c	32	22	71.0	1178	3	US-09-270-767-29091	Sequence 29091, A
c	33	22	71.0	1215	3	US-08-952-899-3	Sequence 3, Appli
	34	22	71.0	1215	3	US-09-328-352-4056	Sequence 4056, Ap
c	35	22	71.0	1332	3	US-08-952-899-1	Sequence 1, Appli
c	36	22	71.0	1479	3	US-09-248-796A-4621	Sequence 4621, Ap
c	37	22	71.0	1485	2	US-07-702-771-2	Sequence 2, Appli
c	38	22	71.0	1485	2	US-08-438-883-2	Sequence 2, Appli
c	39	22	71.0	1485	2	US-08-741-599-2	Sequence 2, Appli
c	40	22	71.0	1514	3	US-08-675-816-1	Sequence 1, Appli
	41	22	71.0	1530	3	US-09-248-796A-5928	Sequence 5928, Ap
	42	22	71.0	2069	3	US-09-276-438-8	Sequence 8, Appli
c	43	22	71.0	2103	3	US-09-270-767-13179	Sequence 13179, A
c	44	22	71.0	2229	3	US-10-104-047-450	Sequence 450, App
c	45	22	71.0	2312	2	US-07-736-178C-1	Sequence 1, Appli
c	46	22	71.0	2685	2	US-08-935-450-5	Sequence 5, Appli
c	47	22	71.0	2685	3	US-09-338-123-5	Sequence 5, Appli
c	48	22	71.0	3191	3	US-08-675-816-3	Sequence 3, Appli
	49	22	71.0	4043	3	US-09-710-279-3354	Sequence 3354, Ap

```
                          GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:            August 11, 2006, 08:01:40 ; Search time 34.875 Seconds
                                               (without alignments)
                                               77.805 Million cell updates/sec

Title:             US-10-072-159-1
Perfect score:     31
Sequence:          1 FXXXXXXXXXXXXXXXXXXFXXXXXGXYXFXX 31


Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5


Searched:          650591 seqs, 87530628 residues


Total number of hits satisfying chosen parameters:      650591


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries


Database :         Issued_Patents_AA:*
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                   2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
                   3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
                   4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
                   5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                   6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                   7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*


      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.


                              SUMMARIES
              %
Result        Query
  No.  Score  Match Length DB  ID                        Description
------------------------------------------------------------------------------
     1    22   71.0   266  2   US-09-710-279-2066        Sequence 2066, Ap
     2    22   71.0   268  2   US-09-252-991A-18273      Sequence 18273, A
     3    22   71.0   292  2   US-09-134-001C-4142       Sequence 4142, Ap
     4    22   71.0   305  2   US-09-328-352-6069        Sequence 6069, Ap
     5    22   71.0   404  2   US-09-328-352-8182        Sequence 8182, Ap
     6    21   67.7   156  2   US-09-198-452A-698        Sequence 698, App
     7    21   67.7   156  2   US-09-438-185A-662        Sequence 662, App
     8    21   67.7   201  1   US-08-801-740-6           Sequence 6, Appli
     9    21   67.7   201  1   US-08-801-740-7           Sequence 7, Appli
    10    21   67.7   201  2   US-08-801-740-6           Sequence 6, Appli
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11	21	67.7	201	2	US-08-801-740-7	Sequence 7, Appli
12	21	67.7	252	2	US-09-252-991A-30813	Sequence 30813, A
13	21	67.7	270	2	US-09-902-540-13092	Sequence 13092, A
14	21	67.7	450	2	US-09-489-039A-10052	Sequence 10052, A
15	21	67.7	1233	2	US-09-134-000C-4971	Sequence 4971, Ap
16	21	67.7	1416	2	US-09-071-035-404	Sequence 404, App
17	21	67.7	1416	2	US-10-206-576-404	Sequence 404, App
18	21	67.7	1448	2	US-09-071-035-402	Sequence 402, App
19	21	67.7	1448	2	US-10-206-576-402	Sequence 402, App
20	20	64.5	63	1	US-08-637-759B-501	Sequence 501, App
21	20	64.5	63	2	US-08-871-355A-501	Sequence 501, App
22	20	64.5	63	2	US-09-201-945-501	Sequence 501, App
23	20	64.5	63	2	US-09-714-602-501	Sequence 501, App
24	20	64.5	86	2	US-09-178-093B-34	Sequence 34, Appl
25	20	64.5	110	2	US-09-270-767-44692	Sequence 44692, A
26	20	64.5	142	1	US-08-997-080-47	Sequence 47, Appl
27	20	64.5	142	1	US-08-997-362-47	Sequence 47, Appl
28	20	64.5	142	2	US-08-873-970-47	Sequence 47, Appl
29	20	64.5	142	2	US-09-095-855-47	Sequence 47, Appl
30	20	64.5	142	2	US-08-705-347A-47	Sequence 47, Appl
31	20	64.5	142	2	US-09-324-542-47	Sequence 47, Appl
32	20	64.5	142	2	US-09-205-426-47	Sequence 47, Appl
33	20	64.5	142	2	US-09-200-643-47	Sequence 47, Appl
34	20	64.5	143	2	US-08-685-808-2	Sequence 2, Appli
35	20	64.5	143	2	US-08-505-860C-2	Sequence 2, Appli
36	20	64.5	162	1	US-08-606-143-44	Sequence 44, Appl
37	20	64.5	226	2	US-09-270-767-44619	Sequence 44619, A
38	20	64.5	229	2	US-09-270-767-56999	Sequence 56999, A
39	20	64.5	312	2	US-09-543-681A-5883	Sequence 5883, Ap
40	20	64.5	329	2	US-09-248-796A-16263	Sequence 16263, A
41	20	64.5	336	2	US-08-987-691A-5	Sequence 5, Appli
42	20	64.5	408	2	US-09-252-991A-33131	Sequence 33131, A
43	20	64.5	421	2	US-10-012-231A-234	Sequence 234, App
44	20	64.5	421	2	US-10-015-389A-234	Sequence 234, App
45	20	64.5	421	2	US-10-006-768A-234	Sequence 234, App
46	20	64.5	421	2	US-10-015-671A-234	Sequence 234, App
47	20	64.5	421	2	US-10-015-393A-234	Sequence 234, App
48	20	64.5	421	2	US-10-011-833A-234	Sequence 234, App
49	20	64.5	421	2	US-10-006-041A-234	Sequence 234, App
50	20	64.5	421	2	US-10-012-064A-234	Sequence 234, App
51	20	64.5	421	2	US-10-015-392A-234	Sequence 234, App
52	20	64.5	421	3	US-10-011-795B-234	Sequence 234, App
53	20	64.5	421	3	US-10-015-386A-234	Sequence 234, App
54	20	64.5	421	3	US-10-012-121A-234	Sequence 234, App
55	20	64.5	421	3	US-10-006-485A-234	Sequence 234, App
56	20	64.5	421	3	US-10-006-746A-234	Sequence 234, App
57	20	64.5	421	3	US-10-012-752A-234	Sequence 234, App
58	20	64.5	421	3	US-10-017-253A-234	Sequence 234, App
59	20	64.5	421	3	US-10-015-519A-234	Sequence 234, App
60	20	64.5	421	3	US-10-015-715A-234	Sequence 234, App
61	20	64.5	421	3	US-10-007-236A-234	Sequence 234, App
62	20	64.5	429	2	US-09-922-501-10	Sequence 10, Appl
63	20	64.5	448	2	US-09-361-443-4	Sequence 4, Appli
64	20	64.5	451	2	US-09-902-540-15200	Sequence 15200, A
65	20	64.5	462	2	US-09-583-110-3587	Sequence 3587, Ap
66	20	64.5	467	2	US-09-361-443-2	Sequence 2, Appli
67	20	64.5	469	2	US-09-198-452A-793	Sequence 793, App

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OM protein - protein search, using sw model

Run on: August 11, 2006, 08:18:16 ; Search time 195.3 Seconds
                                            (without alignments)
                                            73.526 Million cell updates/sec

Title: US-10-072-159-1
Perfect score: 31
Sequence: 1 FXXXXXXXXXXXXXXXXXXFXXXXXGXYXFXX 31

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_AA_Main:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                   SUMMARIES

          %
Result   Query
  No.   Score Match Length DB ID   Description
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      1   22   71.0   119   4 US-10-434-156-17   Sequence 17, Appl
      2   22   71.0   136   4 US-10-434-156-22   Sequence 22, Appl
      3   22   71.0   163   3 US-09-030-847-2   Sequence 2, Appli
      4   22   71.0   163   4 US-10-215-088-2   Sequence 2, Appli
      5   22   71.0   163   4 US-10-775-165-2   Sequence 2, Appli
      6   22   71.0   215   3 US-09-030-847-4   Sequence 4, Appli
      7   22   71.0   215   4 US-10-215-088-4   Sequence 4, Appli
      8   22   71.0   215   4 US-10-170-385-289   Sequence 289, App
      9   22   71.0   215   4 US-10-775-165-4   Sequence 4, Appli
     10   22   71.0   219   4 US-10-276-774-2150   Sequence 2150, Ap
     11   22   71.0   266   5 US-10-793-626-2066   Sequence 2066, Ap

12	22	71.0	278	5	US-10-732-923-858	Sequence 858, App
13	22	71.0	292	4	US-10-724-972A-4167	Sequence 4167, Ap
14	22	71.0	296	4	US-10-282-122A-67003	Sequence 67003, A
15	22	71.0	302	4	US-10-282-122A-77397	Sequence 77397, A
16	22	71.0	374	4	US-10-437-963-159816	Sequence 159816,
17	22	71.0	440	6	US-11-087-099-5856	Sequence 5856, Ap
18	22	71.0	636	4	US-10-425-114-68352	Sequence 68352, A
19	22	71.0	636	4	US-10-425-115-274242	Sequence 274242,
20	22	71.0	1421	4	US-10-424-599-275109	Sequence 275109,
21	22	71.0	1678	4	US-10-437-963-126095	Sequence 126095,
22	22	71.0	1730	4	US-10-424-599-275110	Sequence 275110,
23	22	71.0	3705	4	US-10-282-122A-77944	Sequence 77944, A
24	21	67.7	53	4	US-10-029-386-29069	Sequence 29069, A
25	21	67.7	71	4	US-10-425-115-272794	Sequence 272794,
26	21	67.7	71	4	US-10-425-115-279228	Sequence 279228,
27	21	67.7	79	4	US-10-424-599-240256	Sequence 240256,
28	21	67.7	83	4	US-10-424-599-168732	Sequence 168732,
29	21	67.7	100	4	US-10-425-115-364312	Sequence 364312,
30	21	67.7	107	6	US-11-096-568A-16598	Sequence 16598, A
31	21	67.7	128	4	US-10-466-242-51	Sequence 51, Appl
32	21	67.7	131	4	US-10-767-701-42874	Sequence 42874, A
33	21	67.7	150	4	US-10-437-963-154089	Sequence 154089,
34	21	67.7	156	4	US-10-289-762-698	Sequence 698, App
35	21	67.7	156	4	US-10-282-122A-54708	Sequence 54708, A
36	21	67.7	156	4	US-10-425-115-333955	Sequence 333955,
37	21	67.7	158	4	US-10-425-115-333946	Sequence 333946,
38	21	67.7	158	6	US-11-096-568A-16597	Sequence 16597, A
39	21	67.7	165	4	US-10-425-114-44317	Sequence 44317, A
40	21	67.7	201	3	US-09-833-245-2073	Sequence 2073, Ap
41	21	67.7	201	3	US-09-833-245-2075	Sequence 2075, Ap
42	21	67.7	201	3	US-09-833-245-2076	Sequence 2076, Ap
43	21	67.7	201	4	US-10-039-865-6	Sequence 6, Appli
44	21	67.7	201	4	US-10-039-865-7	Sequence 7, Appli
45	21	67.7	201	4	US-10-060-255-59	Sequence 59, Appl
46	21	67.7	201	4	US-10-060-255-68	Sequence 68, Appl
47	21	67.7	201	4	US-10-060-255-69	Sequence 69, Appl
48	21	67.7	201	4	US-10-408-765A-717	Sequence 717, App
49	21	67.7	201	5	US-10-881-088-59	Sequence 59, Appl
50	21	67.7	201	5	US-10-881-088-68	Sequence 68, Appl
51	21	67.7	201	5	US-10-881-088-69	Sequence 69, Appl
52	21	67.7	201	5	US-10-287-436A-456	Sequence 456, App
53	21	67.7	201	5	US-10-287-436A-1258	Sequence 1258, Ap
54	21	67.7	201	6	US-11-264-096-2073	Sequence 2073, Ap
55	21	67.7	201	6	US-11-264-096-2075	Sequence 2075, Ap
56	21	67.7	201	6	US-11-264-096-2076	Sequence 2076, Ap
57	21	67.7	208	4	US-10-425-115-321090	Sequence 321090,
58	21	67.7	210	4	US-10-335-977-5883	Sequence 5883, Ap
59	21	67.7	210	4	US-10-335-977-5884	Sequence 5884, Ap
60	21	67.7	215	4	US-10-335-977-5885	Sequence 5885, Ap
61	21	67.7	233	4	US-10-424-599-165427	Sequence 165427,
62	21	67.7	238	4	US-10-282-122A-58562	Sequence 58562, A
63	21	67.7	271	5	US-10-667-295-98	Sequence 98, Appl
64	21	67.7	277	4	US-10-225-066A-370	Sequence 370, App
65	21	67.7	277	4	US-10-374-780A-2724	Sequence 2724, Ap
66	21	67.7	277	5	US-10-732-923-5393	Sequence 5393, Ap
67	21	67.7	277	5	US-10-225-066A-370	Sequence 370, App
68	21	67.7	277	5	US-10-667-295-97	Sequence 97, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 11, 2006, 22:56:56 ; Search time 151 Seconds
                                           (without alignments)
                                           2416.333 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK..........YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
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       Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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5	708	100.0	4517	3	US-09-909-547-5	Sequence 5, Appli
6	708	100.0	4517	4	US-10-231-814-5	Sequence 5, Appli
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ALIGNMENTS

GenCore version 5.1.9
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Run on: August 11, 2006, 23:26:35 ; Search time 174 Seconds
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Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


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     6    708   100.0   244   2  US-09-336-536-20           Sequence 20, Appl
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; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET.036APC
; CURRENT APPLICATION NUMBER: US/09/485,316A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT IB98/01256

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                           GenCore version 5.1.9
                   Copyright (c) 1993 - 2006  Biocceleration Ltd.


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Run on:            August 11, 2006, 08:35:41 ; Search time 33 Seconds
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Post-processing: Minimum Match 0%
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21     98.5   13.9     350   7   US-11-147-397-41          Sequence 41, Appl
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24     74     10.5     370   6   US-10-953-349-16808       Sequence 16808, A
25     74     10.5     370   7   US-11-056-355B-53965      Sequence 53965, A
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32     67.5    9.5     294   6   US-10-953-349-10083       Sequence 10083, A
33     67.5    9.5     552   6   US-10-509-131-50          Sequence 50, Appl
34     67.5    9.5     563   6   US-10-509-131-40          Sequence 40, Appl
35     67      9.5     362   7   US-11-330-403-18262       Sequence 18262, A
36     66.5    9.4     555   7   US-11-330-403-4956        Sequence 4956, Ap
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38     66      9.3     216   7   US-11-056-355B-64569      Sequence 64569, A
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ALIGNMENTS

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; Sequence 2, Application US/10514715
; Publication No. US20060166873A1
; GENERAL INFORMATION:
; APPLICANT: KADOWAKI, TAKASHI
; APPLICANT: YAMAUCHI, TOSHIMASA
; APPLICANT: KUBOTA, NAOTO
; APPLICANT: TERAUCHI, YASUO
; APPLICANT: KUBOTA, TETSUYA
; APPLICANT: NODA, TETSUO
; APPLICANT: NAGAI, RYOZO
; APPLICANT: IMAI, YASUSHI
; TITLE OF INVENTION: PREVENTIVE/REMEDY FOR ARTERIOSCLEROSIS
; FILE REFERENCE: 262193US0PCT
; CURRENT APPLICATION NUMBER: US/10/514,715

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

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Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
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        Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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c	6	16	100.0	18	2	US-08-379-081B-2	Sequence 2, Appli
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c	22	16	100.0	18	2	US-08-379-081B-18	Sequence 18, Appl
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GenCore version 5.1.9
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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
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     and is derived by analysis of the total score distribution.

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     5   16   100.0   23 1   US-08-056-200-57   Sequence 57, Appl
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